

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/566,224  
Source: IFWP  
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IFWP

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION: US/10/566,224**

**DATE: 02/03/2006**  
**TIME: 11:00:25**

**Input Set : A:\PTO.TS1.txt**  
**Output Set: N:\CRF4\02032006\J566224.raw**

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3 <110> APPLICANT: FUJII, Kazutoshi
4     IIBOSHI, Masae
5     YANASE, Michiyo
6     TAKATA, Hiroki
7     TAKAHA, Takeshi
8     KURIKI, Takashi
10 <120> TITLE OF INVENTION: A METHOD FOR IMPROVING THE THERMOSTABILITY OF
SUCROSEPHOSPHORYLASE (SP)
12 <130> FILE REFERENCE: EG014US
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/566,224
C--> 15 <141> CURRENT FILING DATE: 2006-01-27
17 <150> PRIOR APPLICATION NUMBER: JP2003-313305
18 <151> PRIOR FILING DATE: 2003-09-04
20 <160> NUMBER OF SEQ ID NOS: 27
22 <170> SOFTWARE: PatentIn version 3.3
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1443
26 <212> TYPE: DNA
27 <213> ORGANISM: Streptococcus mutans
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (1)..(1443)
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36 Met Pro Ile Thr Asn Lys Thr Met Leu Ile Thr Tyr Ala Asp Ser Leu
37 1          5          10          15
39 ggt aaa aat ttg aaa gaa ttg aat gaa aat att gag aat tat ttt gga      96
40 Gly Lys Asn Leu Lys Glu Leu Asn Glu Asn Ile Glu Asn Tyr Phe Gly
41          20          25          30
43 gat gct gtt ggc ggt gtc cat ttg ctg cca ttc ttt cct tcc aca ggt    144
44 Asp Ala Val Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly
45          35          40          45
47 gat cgt ggc ttt gca ccg att gat tac cat gaa gtt gac tct gct ttt    192
48 Asp Arg Gly Phe Ala Pro Ile Asp Tyr His Glu Val Asp Ser Ala Phe
49          50          55          60
51 ggc gat tgg gat gtc aaa cgt ttg ggt gaa aaa tat tac ctc atg      240
52 Gly Asp Trp Asp Asp Val Lys Arg Leu Gly Glu Lys Tyr Tyr Leu Met
53 65          70          75          80
55 ttt gat ttc atg att aat cat att tcg cgt cag tct aaa tat tat aaa    288
56 Phe Asp Phe Met Ile Asn His Ile Ser Arg Gln Ser Lys Tyr Tyr Lys
57          85          90          95
59 gat tac caa gaa aag cat gaa gca agt gct tat aaa gat cta ttt tta    336
60 Asp Tyr Gln Glu Lys His Glu Ala Ser Ala Tyr Lys Asp Leu Phe Leu
61          100         105         110

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63	aat tgg gat aaa ttt tgg cct aaa aat cgc ccg aca caa gaa gat gtg	384
64	Asn Trp Asp Lys Phe Trp Pro Lys Asn Arg Pro Thr Gln Glu Asp Val	
65	115 120 125	
67	gac ctg att tat aag cgt aag gat cga gca cct aag cag gaa atc caa	432
68	Asp Leu Ile Tyr Lys Arg Lys Asp Arg Ala Pro Lys Gln Glu Ile Gln	
69	130 135 140	
71	ttt gca gat ggc agt gtt gaa cat ctc tgg aac act ttt ggg gag gaa	480
72	Phe Ala Asp Gly Ser Val Glu His Leu Trp Asn Thr Phe Gly Glu Glu	
73	145 150 155 160	
75	cag att gat ctt gac gtg act aaa gaa gtg act atg gat ttt att cgc	528
76	Gln Ile Asp Leu Asp Val Thr Lys Glu Val Thr Met Asp Phe Ile Arg	
77	165 170 175	
79	tct acc att gaa aat tta gca gcc aac ggc tgt gat ctc att cgt ttg	576
80	Ser Thr Ile Glu Asn Leu Ala Ala Asn Gly Cys Asp Leu Ile Arg Leu	
81	180 185 190	
83	gat gcc ttt gct tat gct gtt aaa aag cta gat acg aat gat ttc ttt	624
84	Asp Ala Phe Ala Tyr Ala Val Lys Lys Leu Asp Thr Asn Asp Phe Phe	
85	195 200 205	
87	gtt gaa cct gaa atc tgg act ctg cta gat aaa gtt cgt gat ata gct	672
88	Val Glu Pro Glu Ile Trp Thr Leu Leu Asp Lys Val Arg Asp Ile Ala	
89	210 215 220	
91	gct gta tcg ggt gcg gaa atc ttg ccg gaa att cat gaa cac tat act	720
92	Ala Val Ser Gly Ala Glu Ile Leu Pro Glu Ile His Glu His Tyr Thr	
93	225 230 235 240	
95	att caa ttt aaa att gca gac cat gat tac tat gtt tat gat ttt gcc	768
96	Ile Gln Phe Lys Ile Ala Asp His Asp Tyr Tyr Val Tyr Asp Phe Ala	
97	245 250 255	
99	ctg cct atg gtg acg ctc tac agc cta tat tcg ggc aag gtt gac cgt	816
100	Leu Pro Met Val Thr Leu Tyr Ser Leu Tyr Ser Gly Lys Val Asp Arg	
101	260 265 270	
103	ctt gcc aaa tgg ctg aaa atg agt ccg atg aaa cag ttc acc acc ctt	864
104	Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gln Phe Thr Thr Leu	
105	275 280 285	
107	gat aca cat gac ggt att ggt gtg gtt gat gtt aag gat atc ctg act	912
108	Asp Thr His Asp Gly Ile Gly Val Val Asp Val Lys Asp Ile Leu Thr	
109	290 295 300	
111	gac gaa att acc tat act tct aat gag ctt tat aag gtc ggt gcc	960
112	Asp Glu Glu Ile Thr Tyr Thr Ser Asn Glu Leu Tyr Lys Val Gly Ala	
113	305 310 315 320	
115	aat gtc aat cgt aag tat tca act gcc gaa tat aat aac ttg gat atc	1008
116	Asn Val Asn Arg Lys Tyr Ser Thr Ala Glu Tyr Asn Asn Leu Asp Ile	
117	325 330 335	
119	tat caa att aat tca act tac tat tca gca ctt ggt gat gat gat caa	1056
120	Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Gln	
121	340 345 350	
123	aaa tac ttt ttg gcc cgc ttg ata caa gct ttt gct cca ggt att cca	1104
124	Lys Tyr Phe Leu Ala Arg Leu Ile Gln Ala Phe Ala Pro Gly Ile Pro	
125	355 360 365	
127	cag gtt tat tac gtt ggc ttt tta gct ggc aag aat gat ctt gaa tta	1152

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128 Gln Val Tyr Tyr Val Gly Phe Leu Ala Gly Lys Asn Asp Leu Glu Leu		
129       370	375	380
131 ctg gaa agc act aaa gaa ggc cgc aat atc aac cgt cat tat tat agt		1200
132 Leu Glu Ser Thr Lys Glu Gly Arg Asn Ile Asn Arg His Tyr Tyr Ser		
133 385	390	395      400
135 agt gaa gaa att gct aag gaa gtg aag cgg cca gtt gtc aag gca ctt		1248
136 Ser Glu Glu Ile Ala Lys Glu Val Lys Arg Pro Val Val Lys Ala Leu		
137       405	410	415
139 tta aat ctc ttt act tac cgc aat cag tca gca gct ttt gat ttg gat		1296
140 Leu Asn Leu Phe Thr Tyr Arg Asn Gln Ser Ala Ala Phe Asp Leu Asp		
141       420	425	430
143 ggc cgt att gaa gtg gaa acg cca aat gaa gcg acc att gtc ata gaa		1344
144 Gly Arg Ile Glu Val Glu Thr Pro Asn Glu Ala Thr Ile Val Ile Glu		
145       435	440	445
147 cgt caa aat aaa gat ggc agt cat atc gca aca gca gag att aat ctc		1392
148 Arg Gln Asn Lys Asp Gly Ser His Ile Ala Thr Ala Glu Ile Asn Leu		
149       450	455	460
151 caa gat atg aca tac aga gta aca gaa aat gat caa aca ata agc ttt		1440
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153 465	470	475      480
155 gaa		1443
156 Glu		
160 <210> SEQ ID NO: 2		
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162 <212> TYPE: PRT		
163 <213> ORGANISM: Streptococcus mutans		
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171 Gly Lys Asn Leu Lys Glu Leu Asn Glu Asn Ile Glu Asn Tyr Phe Gly		
172       20	25	30
175 Asp Ala Val Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly		
176       35	40	45
179 Asp Arg Gly Phe Ala Pro Ile Asp Tyr His Glu Val Asp Ser Ala Phe		
180       50	55	60
183 Gly Asp Trp Asp Asp Val Lys Arg Leu Gly Glu Lys Tyr Tyr Leu Met		
184 65	70	75      80
187 Phe Asp Phe Met Ile Asn His Ile Ser Arg Gln Ser Lys Tyr Tyr Lys		
188       85	90	95
191 Asp Tyr Gln Glu Lys His Glu Ala Ser Ala Tyr Lys Asp Leu Phe Leu		
192       100	105	110
195 Asn Trp Asp Lys Phe Trp Pro Lys Asn Arg Pro Thr Gln Glu Asp Val		
196       115	120	125
199 Asp Leu Ile Tyr Lys Arg Lys Asp Arg Ala Pro Lys Gln Glu Ile Gln		
200       130	135	140
203 Phe Ala Asp Gly Ser Val Glu His Leu Trp Asn Thr Phe Gly Glu Glu		
204 145	150	155      160
207 Gln Ile Asp Leu Asp Val Thr Lys Glu Val Thr Met Asp Phe Ile Arg		
208       165	170	175

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211 Ser Thr Ile Glu Asn Leu Ala Ala Asn Gly Cys Asp Leu Ile Arg Leu  
212 180 185 190  
215 Asp Ala Phe Ala Tyr Ala Val Lys Lys Leu Asp Thr Asn Asp Phe Phe  
216 195 200 205  
219 Val Glu Pro Glu Ile Trp Thr Leu Leu Asp Lys Val Arg Asp Ile Ala  
220 210 215 220  
223 Ala Val Ser Gly Ala Glu Ile Leu Pro Glu Ile His Glu His Tyr Thr  
224 225 230 235 240  
227 Ile Gln Phe Lys Ile Ala Asp His Asp Tyr Tyr Val Tyr Asp Phe Ala  
228 245 250 255  
231 Leu Pro Met Val Thr Leu Tyr Ser Leu Tyr Ser Gly Lys Val Asp Arg  
232 260 265 270  
235 Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gln Phe Thr Thr Leu  
236 275 280 285  
239 Asp Thr His Asp Gly Ile Gly Val Val Asp Val Lys Asp Ile Leu Thr  
240 290 295 300  
243 Asp Glu Glu Ile Thr Tyr Thr Ser Asn Glu Leu Tyr Lys Val Gly Ala  
244 305 310 315 320  
247 Asn Val Asn Arg Lys Tyr Ser Thr Ala Glu Tyr Asn Asn Leu Asp Ile  
248 325 330 335  
251 Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Asp Gln  
252 340 345 350  
255 Lys Tyr Phe Leu Ala Arg Leu Ile Gln Ala Phe Ala Pro Gly Ile Pro  
256 355 360 365  
259 Gln Val Tyr Tyr Val Gly Phe Leu Ala Gly Lys Asn Asp Leu Glu Leu  
260 370 375 380  
263 Leu Glu Ser Thr Lys Glu Gly Arg Asn Ile Asn Arg His Tyr Tyr Ser  
264 385 390 395 400  
267 Ser Glu Glu Ile Ala Lys Glu Val Lys Arg Pro Val Val Lys Ala Leu  
268 405 410 415  
271 Leu Asn Leu Phe Thr Tyr Arg Asn Gln Ser Ala Ala Phe Asp Leu Asp  
272 420 425 430  
275 Gly Arg Ile Glu Val Glu Thr Pro Asn Glu Ala Thr Ile Val Ile Glu  
276 435 440 445  
279 Arg Gln Asn Lys Asp Gly Ser His Ile Ala Thr Ala Glu Ile Asn Leu  
280 450 455 460  
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292 <211> LENGTH: 1434  
293 <212> TYPE: DNA  
294 <213> ORGANISM: Streptococcus pneumoniae  
297 <220> FEATURE:  
298 <221> NAME/KEY: CDS  
299 <222> LOCATION: (1)..(1434)  
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303 Met Pro Ile Gln Asn Lys Thr Met Leu Ile Thr Tyr Ser Asp Ser Leu

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Input Set : A:\PTO.TS1.txt  
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304	1	5	10	15													
306	gga	aat	aat	ctt	aaa	gac	tta	tat	gat	aat	ttg	gaa	gag	cat	ttt	gga	96
307	Gly	Asn	Asn	Leu	Lys	Asp	Leu	Tyr	Asp	Asn	Leu	Glu	Glu	His	Phe	Gly	
308	20										25				30		
310	gat	gct	att	gga	gga	gtt	cac	ctt	tta	cca	ttt	ttc	cca	tca	aca	gtt	144
311	Asp	Ala	Ile	Gly	Gly	Val	His	Leu	Leu	Pro	Phe	Phe	Pro	Ser	Thr	Val	
312	35									40				45			
314	gat	cgt	gga	ttt	gcg	cca	gtt	gac	tac	gac	gaa	gtg	gac	tca	gct	ttt	192
315	Asp	Arg	Gly	Phe	Ala	Pro	Val	Asp	Tyr	Asp	Glu	Val	Asp	Ser	Ala	Phe	
316	50									55				60			
318	ggg	gtt	gat	tgg	gag	gtt	aag	cgt	tta	ggt	gag	aaa	tat	tat	ctt	atg	240
319	Gly	Asp	Trp	Glu	Asp	Val	Lys	Arg	Leu	Gly	Glu	Lys	Tyr	Tyr	Leu	Met	
320	65									70			75		80		
322	ttt	gat	ttt	atg	att	aat	cat	att	tct	cgt	caa	tcc	aag	tat	tat	aag	288
323	Phe	Asp	Phe	Met	Ile	Asn	His	Ile	Ser	Arg	Gln	Ser	Lys	Tyr	Tyr	Lys	
324	85									90				95			
326	gac	tat	caa	gaa	aaa	cat	gaa	gcc	agt	gaa	ttt	aaa	gct	ctc	ttt	tta	336
327	Asp	Tyr	Gln	Glu	Lys	His	Glu	Ala	Ser	Glu	Phe	Lys	Ala	Leu	Phe	Leu	
328	100									105				110			
330	aac	tgg	gat	aag	ttt	tgg	cca	gaa	aac	cgt	ccg	aca	cag	tct	gat	gta	384
331	Asn	Trp	Asp	Lys	Phe	Trp	Pro	Glu	Asn	Arg	Pro	Thr	Gln	Ser	Asp	Val	
332	115									120				125			
334	gat	tta	att	tac	aag	cgt	aag	gat	cgt	gca	cca	aag	caa	gag	att	gtg	432
335	Asp	Leu	Ile	Tyr	Lys	Arg	Lys	Asp	Arg	Ala	Pro	Lys	Gln	Glu	Ile	Val	
336	130									135				140			
338	ttt	gaa	gat	ggt	tca	gtg	gaa	cat	ttg	tgg	aat	acc	ttt	ggt	gag	gag	480
339	Phe	Glu	Asp	Gly	Ser	Val	Glu	His	Leu	Trp	Asn	Thr	Phe	Gly	Glu	Glu	
340	145									150			155		160		
342	cag	att	gat	ctt	gat	gtg	acc	aaa	gaa	gta	act	atg	gaa	ttt	atc	cgt	528
343	Gln	Ile	Asp	Leu	Asp	Val	Thr	Lys	Glu	Val	Thr	Met	Glu	Phe	Ile	Arg	
344	165									170				175			
346	aag	acc	att	cag	cac	ttg	gca	agt	aat	ggg	tgt	gat	ttg	att	cgt	cta	576
347	Lys	Thr	Ile	Gln	His	Leu	Ala	Ser	Asn	Gly	Cys	Asp	Leu	Ile	Arg	Leu	
348	180									185				190			
350	gat	gcc	ttt	gct	tat	gca	gtg	aag	aaa	ttg	gat	act	aat	gat	ttc	ttt	624
351	Asp	Ala	Phe	Ala	Tyr	Ala	Val	Lys	Lys	Leu	Asp	Thr	Asn	Asp	Phe	Phe	
352	195									200				205			
354	gtg	gaa	cca	gat	att	tgg	gat	tta	ttg	gac	aaa	gtt	cga	gat	atc	gtc	672
355	Val	Glu	Pro	Asp	Ile	Trp	Asp	Leu	Leu	Asp	Lys	Val	Arg	Asp	Ile	Ala	
356	210									215				220			
358	gct	gag	tat	ggg	aca	gag	ctt	tta	cct	gag	att	cat	gaa	cac	tat	tcg	720
359	Ala	Glu	Tyr	Gly	Thr	Glu	Leu	Leu	Pro	Glu	Ile	His	Glu	His	Tyr	Ser	
360	225									230			235		240		
362	att	cag	ttt	aaa	ata	gca	gac	cat	gat	tac	tat	gtt	tat	gat	ttt	gtc	768
363	Ile	Gln	Phe	Lys	Ile	Ala	Asp	His	Asp	Tyr	Tyr	Val	Tyr	Asp	Phe	Ala	
364	245									250				255			
366	ctt	cca	atg	gtg	aca	ctt	tat	act	ctt	tac	agt	tcc	aga	aca	gag	cgt	816
367	Leu	Pro	Met	Val	Thr	Leu	Tyr	Thr	Leu	Tyr	Ser	Ser	Arg	Thr	Glu	Arg	
368	260									265				270			

**VERIFICATION SUMMARY**  
PATENT APPLICATION: US/10/566,224

DATE: 02/03/2006  
TIME: 11:00:26

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L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date